

Is the Freeman-Tukey double arcsine transformation a reliable approach for proportion meta-analysis?

An example with a Living SR on Covid-19 vaccines and Pregnancy outcomes.

Ciapponi A, Bardach A, Glujovsky D, Berrueta M, Castellana N

Trusted evidence. Informed decisions.

abardach@iecs.org.ar @Ariel_Bardach

Better health.

Institute for Clinical Effectiveness and Health Policy

No conflicts of interest



Previous work

Recently questioned...

- Meta-analysis often utilizes pooling of proportions to gain more accurate estimates of disease frequency, such as cumulative incidence or prevalence. They are usually based on transformed proportions using Freeman-Tukey double arcsine transformations (FTT).
- A recent study proposed the use of generalized linear mixed models (GLMM) over FTT, on the premise the latter produces misleading results, sparking controversy.[1]
- However, other authors, using the same set of studies, reanalyzed the data and concluded that the FTT is the most reliable approach and remains the preferred transformation in proportion meta-analysis.[2]
- We aimed to compare the performance of FTT with GLMM in a large set of proportion meta-analyses from an ongoing Living Systematic Review.
- 1. Schwarzer G, Chemaitelly H, Abu-Raddad LJ, Rücker G. Seriously misleading results using inverse of Freeman-Tukey double arcsine transformation in meta-analysis of single proportions. Res Synth Methods. 2019;10: 476–483.
- 2. Doi SA, Xu C. The Freeman-Tukey double arcsine transformation for the meta-analysis of proportions: Recent criticisms were seriously misleading. J Evid Based Med. 2021;14: 259–261.















Stillbirth

O Dose

Vaccine type ☑ RNA

☐ Viral vector

Not specified **Dominant Variant**

Not specified Effect measure

COVID-19 vaccination

Type of Pregnant Population Exposed to

O RR

About

COVID-19 Vaccines for Pregnant

A Living Systematic Review and

Last update was made on 9/3/2023

This is a regularly updated, comprehensive database and synthesis of published literature relating to COVID-19 vaccines in pregnancy. To start your search, click on any given country on the map to see all collected studies or click on the Outcomes tab for details on studies reporting on Maternal Pregnancy Outcomes, Maternal Adverse Events Following Immunization, Infant Safety Outcomes, Vaccine Efficacy/Effectiveness Outcomes, and Immunogenicity. For more information on the Living Systematic Review (LSR) and inclusion criteria, click the Methodology and About tabs. Filters applied: None



COVID 19 vaccines for pregnant persons: a living systematic subgroup analysis Trimester review and meta-analysis O Dominant variant O Vaccine type

https://safeinpregnancy.org/lsr/

















Summary table

We identified 37 studies reporting this outcome. Based on the methodology described, only 4 studies reported adjusted effect measures for this outcome: Dick, A (2022) (a), Fell, D.B. (2022), Hui, L (2022), Magnus, M.C. (2022). Finally, 3 were included in the meta-analysis based on the se filters. The meta-analysis included a total of 84,744 patients exposed to the vaccine in 3 countries: Australia, Canada and Israel.

Maternal safety of COVID-19 vaccines during pregnancy versus unvaccinated pregnant population: Stillbirth.



Methdos

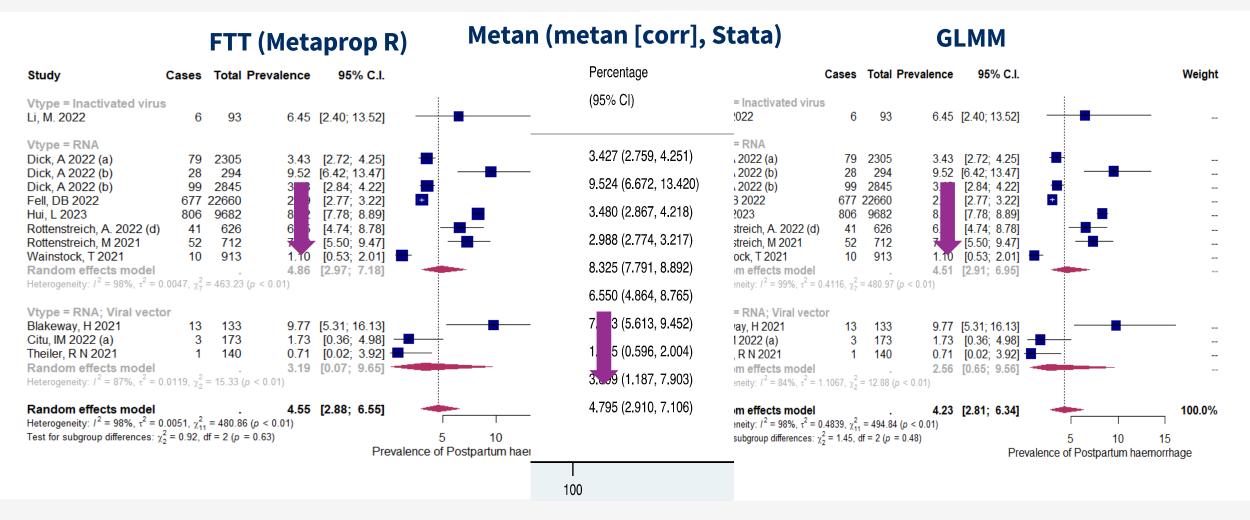
• We conducted GLMM[1] and FTT over a **large dataset** of proportions **from a living systematic review** and meta-analysis about **safety, immunogenicity, and effectiveness of COVID-19 vaccines** for pregnant people (https://safeinpregnancy.org/lsr/) applying recommended safeguards (using corrected statistical packages: Metan in Stata) and other approaches (GLMM and Metaprop in R):

Safeguards:

- a) avoiding the use of the average of the double arcsine and its variance for synthesis;
- b) using the inverse of the variance of the pooled FTT proportion
- c) modifying the confidence intervals to prevent numerical inaccuracies.
- Compared results for MAs with few/several studies, and for Vaccine outcomes/Adverse effects

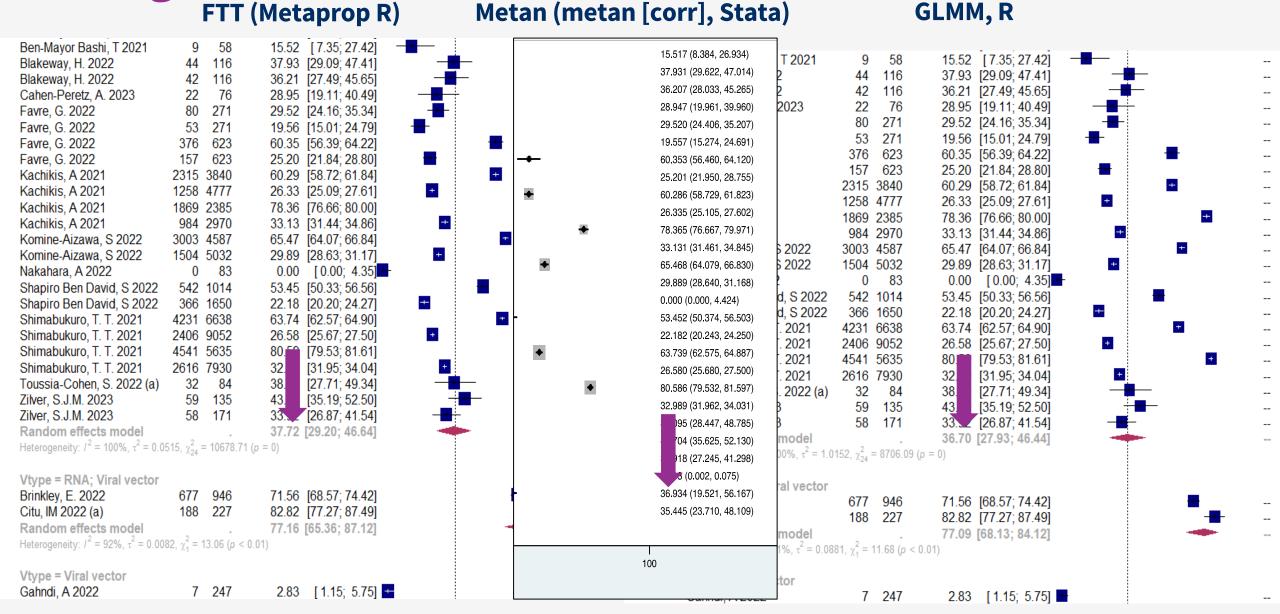


Postpartum Hemorrhage





Fatigue



Stillbirth

FTT (metaprop, R)

Metan (metan [corr], Stata)

GLMM (R)

Study	Cases Total	Prevalence 95% C.I.		studyname	Events per 10 (95% CI)
Vtype = RNA				0.4	
Dick, A 2022 (a)	20 2305	8.68 [5.31; 13.37]	-	S1	→ 8.677 (5.624,
Dick, A 2022 (b)	0 294	0.00 [0.00; 12.47]		S2	← 0.000 (0.000,
Dick, A 2022 (b)	20 2845	7.03 [4.30; 10.84]	<u>:</u> -	S3	→ 7.030 (4.555,
Fell, D.B. 2022	107 43099	2.48 [2.04; 3.00]		S4	2.483 (2.055,
Goldshtein, I 2021	1 7530	0.13 [0.00; 0.74]			
Hui, L 2023	15 9682	1. [0.87; 2.55]	: _	S5	■ 0.133 (0.023,
Rottenstreich, M 2021	5 712	7. [2.28; 16.31]		S6	
Trostle, ME 2021	0 85	0. [0.00; 42.47]		S7	→ 7.022 (3.003)
Vuong, L.N. 2022	1 513	1 [0.05; 10.81]		S8	← → 000 (0.000,
Zilver, S.J.M. 2023	0 130	0.07 [0.00; 27.98]			
Random effects model Heterogeneity: $I^2 = 89\%$, $\tau^2 =$	0.00072 - 70.50	1.95 [0.31; 4.51]		S9	→ 1 49 (0.344,
neterogeneity. 7 – 69%, t –	υ.υυυτ, χ ₉ – το.5ο	(p < 0.01)		S10	← → 00 00 (0.000,
Vtype = RNA; Viral vec	tor			Overall, IVhet	1.380 (0.065,
Blakeway, H 2021	0 133	0.00 [0.00; 27.35]		Overall, DL	2.983 (1.377,
Magnus, M.C. 2022	50 28506	1.75 [1.30; 2.31]		· ·	•
Stock, S. 2021	11 2364	4.65 [2.33; 8.31]	_	$(I^2 = 88.5\%, H =$	2.95)
Theiler, R N 2021	0 140	0.00 [0.00; 26.01]		_	
Random effects model		1.17 [0.00; 3.67]	:		.1 7
Heterogeneity: $I^2 = 55\%$, $\tau^2 =$					
	- 23	,			
Vtype = Viral vector					
Vuong, L.N. 2022	2 441	4.54 [0.55; 16.29]	- 1	5.2%	
Random effects model		1.84 [0.55; 3.65]	<u> </u>	100.0%	
Heterogeneity: $I^2 = 84\%$, $\tau^2 =$			I I	1 1	
Test for subgroup differences:	$\chi_2^2 = 0.75$, df = 2 (p	= 0.69)		30 40	
			Prevalence of S	Stillbirth	

Study	Cases	Total	Prevalence	95% C.I.		
Vtype = RNA						
Dick, A 2022 (a)	20	2305	8.68	[5.31; 13.37]	-	
Dick, A 2022 (b)	0	294	0.00	[0.00; 12.47]		
Dick, A 2022 (b)	20	2845	7.03	[4.30; 10.84]	-	
Fell, D.B. 2022	107	43099				
Goldshtein, I 2021	1	7530	0.13			
Hui, L 2023	15	9682	1.		_	
Rottenstreich, M 2021	5	–				
Trostle, ME 2021	0					
Vuong, L.N. 2022						
	0	130				
				[0.83; 5.05]		
Heterogeneity: $I^2 = 85\%$, $\tau^2 =$	1.2958, χ	= 60.66	(p < 0.01)			
Vtype = RNA; Viral vect	or					
Blakeway, H 2021	0	133	0.00	[0.00; 27.35]		
Magnus, M.C. 2022	50	28506	1.75	[1.30; 2.31]	+	
Stock, S. 2021	11	2364	4.65	[2.33; 8.31]		
Theiler, R N 2021	0	140	0.00	[0.00; 26.01]		
Random effects model			2.38	[1.30; 4.37]	*	
Heterogeneity: $I^2 = 65\%$, $\tau^2 =$	0.1452, χ	$\frac{2}{3} = 8.6 (p)$	= 0.04)			
Vtype = Viral vector						
Vuong, L.N. 2022	2	441	4.54	[0.55; 16.29]		
Random effects model			2 28	[1 22: 4 25]		
Heterogeneity: $I^2 = 82\%$ $\tau^2 =$	ck, A 2022 (a) 20 2305 8.68 [5.31; 13.37]					
Test for subgroup differences:	$\chi_2^2 = 0.92$	df = 2 (p	= 0.63)	() 10	

Table. Summary of MA results per vaccine type subgroup considering FTT and GLMM aproaches

	Subgroup	#studi es	FTT			GLMM				Rel Diff		
Outcome			prop	Prop-95% CI	l ² %	I ² %-95% CI	prop	Prop-95% CI	l ² %	I ² %-95% CI	(%)	Abs Diff
PPH	Inactivated virus	1	6.450	[2.20; 12.50]	NA	NA	6.450	[2.93; 13.62]	NA	NA		
	RNA	8	4.860	[2.97; 7.18]	98.49	[97.95;98.89]	4.510	[2.91; 6.95]	98.54	[98.03;98.92]	7.20	0.350
	RNA; Viral vector	3	3.190	[0.07; 9.65]	86.95	[62.75;95.43]	2.560	[0.65; 9.56]	84.47	[53.74;94.79]	19.75	0.630
Stillbirth	RNA	10	1.945	[0.307; 4.512]	88.55	[81.03;93.09]	2.045	[0.826; 5.053]	85.16	[74.47;91.38]	5.14	0.100
	RNA; Viral vector	4	1.172	[0.001; 3.671]	55.16	[0.00;85.16]	2.380	[1.296; 4.366]	65.11	[0.00;88.15]	103.07	1.208
	Viral vector	1	4.535	[0.068; 13.620]	NA	NA	4.535	[1.135; 17.946]	NA	NA		
Fatigue	RNA	25	37.720	[29.20; 46.64]	99.78	[99.76;99.79]	36.700	[27.93; 46.44]	99.72	[99.70;99.75]	2.70	1.020
	RNA; Viral vector	2	77.160	[65.36; 87.12]	92.34	[73.92;97.75]	77.090	[68.13; 84.12]	91.44	[69.92;97.56]	0.09	0.070
	Viral vector	1	2.830	[1.07; 5.33]	NA	NA	2.830	[1.36; 5.82]	NA	NA		
Apgar	RNA	13	1.260	[0.76; 1.88]	89.38	[83.68;93.09]	1.210	[0.76; 1.91]	80.21	[67.02;88.13]	3.97	0.050
score<7 at five minutes	RNA; Viral vector	3	1.310	[1.17; 1.45]	0.00	[0.00;89.60]	1.510	[1.37; 1.65]	0.00	[0.00;89.60]	15.27	0.200
SAEs	RNA	5	0.254	[0.129; 0.407]	0.00	[0.00;79.20]	0.559	[0.424; 0.737]	0.00	[0.00;79.20]	120.07	0.305
	Viral vector	1	0.405	[0.000; 1.731]	NA	NA	0.405	[0.057; 2.816]	NA	NA		



Conclusions

- We compared methods across different type of outcomes in studies about COVID-19 vaccination in pregnant persons
- FTT continues to be the a valid method under new implementations of statistical software.
- Ensuring the optimal method for conducting meta-analyses of proportions is essential, as it plays a pivotal role in making accurate estimations in epidemiology and guiding decisionmaking processes.



Thank You!

